(i) a polynucleotide capable of hybridizing under high stringency conditions to the nucleic acid of SEQ ID NO: 2, wherein said polynucleotide encodes a polypeptide having an inorganic carbon fixation activity; and

(ii) a plant promoter operable in directing nuclear transcription of said polynucleotide; and

A2 cont'd

(b) selecting from said photosynthetic plants of step (a) a photosynthetic plant comprising cells having at least 5% enhanced inorganic carbon fixation as compared to otherwise similar, non-transformed cells of said photosynthetic plants;

thereby obtaining the photosynthetic plant characterized by enhanced inorganic carbon fixation.

2. (Amended) The method of claim 1, wherein said transforming said cells of the photosynthetic plant with said nucleic acid construct is effected by a method selected from the group consisting of genetic transformation and transient transformation.

6. (Amended) The method of claim 1, wherein said polypeptide having an inorganic carbon fixating activity is at least 90 % homologous to

A3 SEQ ID NO:3 as determined using the Blast software where gap open penalty equals 11, gap extension penalty equals 1 and matrix is blosum 62.

8. (Amended) The method of claim 1, wherein said photosynthetic plant is a C3 plant.

A4 9. (Amended) The method of claim 8, wherein said C3 plant is selected from the group consisting of tobacco, tomato, soybean, potato,

cucumber, cotton, wheat, rice and barley.

A4 cont

10. (Amended) The method of claim 1, wherein said photosynthetic plant is a C4 plant.

13. (Amended) The method of claim 1, wherein said plant promoter is selected from the group consisting of a constitutive plant promoter, a tissue specific plant promoter and an inducible plant promoter.

A5

16. (Amended) A nucleic acid construct for enhancing inorganic carbon fixation by a photosynthetic plant, the nucleic acid construct comprising:

(a) a polynucleotide capable of hybridizing under high stringency conditions to the nucleic acid of SEQ ID NO: 2, wherein said polynucleotide encodes a polypeptide having an inorganic carbon fixation activity; and

A6

(b) a plant promoter being for directing nuclear transcription of said polynucleotide;

wherein expression of said polypeptide in cells of the photosynthetic plant results in at least 5% enhanced inorganic carbon fixation as measured in comparison to otherwise similar, non-transformed cells of the photosynthetic plant.

19. (Amended) The nucleic acid construct of claim 16, wherein said polypeptide having an inorganic carbon fixating activity is at least 90 % homologous to SEQ ID NO:3 as determined using the Blast software where gap open penalty equals 11, gap extension penalty equals 1 and matrix is blosum 62.

A7

20. (Amended) The nucleic acid construct of claim 17, wherein said plant promoter is selected from the group consisting of a constitutive plant

promoter, a tissue specific plant promoter and an inducible plant promoter.

21. The nucleic acid construct of claim 20, wherein:

(i) said constitutive plant promoter is selected from the group consisting of CaMV35S plant promoter, CaMV19S plant promoter, FMV34S plant promoter, sugarcane bacilliform badnavirus plant promoter, CsVMV plant promoter, *Arabidopsis* ACT2/ACT8 actin plant promoter, *Arabidopsis* ubiquitin UBQ1 plant promoter, barley leaf thionin BTH6 plant promoter, and rice actin plant promoter;

(ii) said tissue specific plant promoter is selected from the group consisting of bean phaseolin storage protein plant promoter, DLEC plant promoter, PHSβ plant promoter, zein storage protein plant promoter, conglutin gamma plant promoter from soybean, AT2S1 gene plant promoter, ACT11 actin plant promoter from *Arabidopsis*, napA plant promoter from *Brassica napus* and potato patatin gene plant promoter; and

A7 Cont

(iii) said inducible plant promoter is selected from the group consisting of a light-inducible plant promoter derived from the pea rbcS gene, a plant promoter from the alfalfa rbcS gene, DRE, MYC and MYB plant promoters which are active in drought; INT, INPS, prxEa, Ha hsp17.7G4 and RD21 plant promoters active in high salinity and osmotic stress, and hsr303J and str246C plant promoters active in pathogenic stress.

22. (Amended) The nucleic acid construct of claim 16, further comprising a sequence element selected from the group consisting of an origin

of replication for propagation in bacterial cells, at least one sequence element for integration into a plant's genome, a polyadenylation recognition sequence, a transcription termination signal, a sequence encoding a translation start site, a sequence encoding a translation stop site, plant RNA virus derived sequences, plant DNA virus derived sequences, tumor inducing (Ti) plasmid derived sequences and a transposable element derived sequence.

A7 cont

23. (Amended) A transformed photosynthetic plant comprising the nucleic acid construct of claim 16.

---

26. (Amended) The transformed photosynthetic plant of claim 25, wherein said plant is a C3 plant.

27. (Amended) The transformed photosynthetic plant of claim 26, wherein said C3 plant is selected from the group consisting of tobacco, tomato, soybean, potato, cucumber, cotton, wheat, rice and barley.

A8

28. (Amended) The transformed photosynthetic plant of claim 25, wherein said plant is a C4 plant.

29. (Amended) The transformed photosynthetic plant of claim 28, wherein said C4 plant is selected from the group consisting of corn, sugar cane and sorghum.

30. (Amended) The transformed photosynthetic plant of claim 23, wherein said plant is characterized by a photosynthetic rate at least 10 % higher as compared to a control non-transformed organism under otherwise identical conditions.

REMARKS